

GEORGE MASON UNIVERSITY
COLLEGE OF SCIENCE
BIOLOGY DEPARTMENT SEMINAR
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***“Population genetics of mid-Atlantic striped bass (*Morone saxatilis*):
genetic divergence among Chesapeake Bay tributaries and effective
number of breeders (N_b) from 1970-2006”***

Striped bass (*Morone saxatilis*) are a long-lived anadromous fish of the U.S. mid-Atlantic. The species experienced a steep decline in the 1980s and the 1984 Atlantic Striped Bass Conservation Act became U.S. law with a goal to recover the species from low population sizes. While now considered demographically recovered, little is known about any population genetic impacts of the population decline and recovery. We tested the hypothesis that the precipitous decline and subsequent recovery of N_c reduced N_b and the ratio of genetic-to-census size (N_b/N_c). Approximately 100 striped bass (*Morone saxatilis*) from each of 1970, 1978, 1986 and 1991 cohorts in archived scales as well as young-of-the-year for 1999 and 2006 cohorts were genotyped at seven to 17 loci microsatellite loci. Estimates of N_b based on genetic association between pairs of loci and two-sample temporal methods were in the tens to low thousands in the recent past and remained approximately constant since 1970. Longer-term estimates of N_e made via coalescent estimates of the effective mutation rate ($4N_e\mu$) were of order thousand to ten thousand and larger than N_b in the recent past. N_b/N_c was of order 1×10^{-5} based on genetic association and temporal estimates of N_b , showing that genetic drift was strong despite large census size. The 1980s N_c decline was not a marked genetic bottleneck, with no impact on allelic richness or N_b given confidence intervals, partly because N_b was consistently low across the entire time period. Despite a demographic recovery, low N_b and N_b/N_c highlight the need to monitor population genetic parameters in this species.

**TUESDAY November 4, 2014
3:00-4:15 PM
Johnson Center Room 334 Meeting Room E**